

FIGURE 1

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SEQ ID NO:39  MYYHVRPKHAL-----FLAFYCYFS-----
SEQ ID NO:40  MKATLAAPSSLTSL-P-----YRTNSS-FGSKSSLLFRSPSSSSSVS-MTTTRGNV
SEQ ID NO:38  MAN-----SXRPA-PLTPLHLRLDAAPPRPSLGHAAARPVPRVPLLLPAR-XLRAPDGV
SEQ ID NO:28  MATVVRI-----PTISCIHIHTFRSQSPRTFARIRVGPWSWAPIRASA-ASSERGEI
SEQ ID NO:08  MATVVRI-----PTISCIHIHTFRSQSPRTFARIRVGPWSWAPIRASA-ASSERGEI
SEQ ID NO:22  MAHAALLHCSQSSR-SLAACRRGSHYRAPSH-VPRHSRRLRRRAVVSL--R-PMASSTA-
SEQ ID NO:24  AR--VQPTGALAPLHPLLRCTSRHLCASASPRAGLCLHHHRRRRRRSRRTKLAVRAMAPT
SEQ ID NO:26  FRH-----GH-----AL-----
1
60

SEQ ID NO:39  LLTMASATIASADLYEKIKNFYDDSSGLWEDVWGEHMHGYYGPHGTYRI---DRRQAQI
SEQ ID NO:40  AVAAAAATSTEALRKGIAEFYNETSGLWEIWDHMHGFGYDPDSSVQLSDSGHKEAQI
SEQ ID NO:38  VDRGPGDAAPGLKEGIAGLYDESSGLWESIWEHMHGFGYDSGEAASMSD--HRRRAQI
SEQ ID NO:28  VLEQPKKDDKKLQKIGIAEFYDESSGLWENIWDHMHGFGYDSDTVSLSD--HRAAQI
SEQ ID NO:08  VLEQPKKDDKKLQKIGIAEFYDESSGLWENIWDHMHGFGYDSDTVSLSD--HRAAQI
SEQ ID NO:22  ---QAPATAAPGLKEGIAGLYDESSGLWENIWDHMHGFGYDSSEAAASMD--HRRRAQI
SEQ ID NO:24  LSSSTAAAAPGLKEGIAGLYDESSGVWESIWEHMHGFGYDAGEAASMSD--HRRRAQI
SEQ ID NO:26  -----
61
120

SEQ ID NO:39  DLIKELLAWAVPQNSA----KPRKILDLCGGIGGSSLYLAQQHQAQAEVMGASLSPVQVERA
SEQ ID NO:40  RMIEESLRFAGVTDEEE-EKKIKKVVDVCGGIGGSSRYLASKFGAECIGITLSPVQAKRA
SEQ ID NO:38  RMIEEALAFAAVP--DDPTNKPTIVDVCGGIGGSSRYLANKYGAQCSGITLSPVQAERG
SEQ ID NO:28  RMIQESLRFASV--SEERSKWPKSIVDVCGGIGGSSRYLAKKFGATSVGITLSPVQAQRA
SEQ ID NO:08  RMIQESLRFASV--SEERSKWPKSIVDVCGGIGGSSRYLAKKFGATSVGITLSPVQAQRA
SEQ ID NO:22  RMIEEALAFAGVPASDDPEKTPKTIVDVCGGIGGSSRYLAKKYGXQCTGITLSPVQAERG
SEQ ID NO:24  RMIEESLAF-----
SEQ ID NO:26  -----
121
180
```

FIGURE 1

| | | |
|--------------|---|-----|
| SEQ ID NO:39 | GERARALGLGSTCQFQVANALDLPFASDSFDWVWSLESGEHMPNKAQFLQEAWRVLKPGG | |
| SEQ ID NO:40 | NDLAAAQSLSHKASFQVADALDQPFEDGKFDLVWSMESGEHMPDKAKFVKELVRVAAPGG | |
| SEQ ID NO:38 | NALAAAQGLSDKASFQVADALEQPFDPGQFDLVWSMESGEHMPNKKFVSELARVAAPGA | |
| SEQ ID NO:28 | NALAAAQGLADKVSFQVADALQPFSDGQFDLVWSMESGEHMPDKAKFVGELARVAAPGA | |
| SEQ ID NO:08 | NALAAAQGLADKVSFQVADALQPFSDGQFDLVWSMESGEHMPDKAKFVGELARVAAPGA | |
| SEQ ID NO:22 | NALAAAQGLSDQVTLQVADALEQPFDPGQFDLVWSMESGEHMPDKRKFSSELARVAAPGG | |
| SEQ ID NO:24 | ----- | |
| SEQ ID NO:26 | -----AQPFDPGQFDLVWSMESDEHMPDKRQFVSELARVAAPGA | 240 |
| | | 181 |
| SEQ ID NO:39 | RLILATWCHRPIDPGNGPLTADERRHLQAIYDVYCLPYVVSPLPDYEAIARECGFGEIKTA | |
| SEQ ID NO:40 | RIIIVTWCHRNLSAGEEALQPEQNILDKICKTFYLPWCSTDDYVNLQSHSLQDIKCA | |
| SEQ ID NO:38 | TIIIVTWCHRNLPSEDSLKPDELNLLKKICDAYYLPDWCSPSDYVVKIAESLSLEDIKTA | |
| SEQ ID NO:28 | IIIIIVTWCHRDLPDEQSLHPWEQDLLKKICDAYYLPWCSTSDYVKKLQSLQSLQDIKSE | |
| SEQ ID NO:08 | IIIIIVTWCHRDLPDEQSLHPWEQDLLKKICDAYYLPWCSTSDYVKKLQSLQSLQDIKSE | |
| SEQ ID NO:22 | TIIIVTWCHRNLDPSETSLKPDELNLLRRICDAYYLPDWCSPSDYVNIAKSLSLEDIKTA | |
| SEQ ID NO:24 | ----- | |
| SEQ ID NO:26 | RIIIVTWCHRNLEPSEESLKPDELNLLKRICDAYYLPDWCSPSDYVVKIAESLSLEDIRTA | 300 |
| | | 241 |
| SEQ ID NO:39 | DWSVAVAPFWDRVIESAFDPRVLWALGQAGPKIINAAALCLRLMKWYERGLVRFGLLTGI | |
| SEQ ID NO:40 | DWSENVAPFWPFAVIRTAALTWKGLVSLRSGMKSIKALTMPMLMIEGYKKGVIKFGIITCQ | |
| SEQ ID NO:38 | DWSENVAPFWPFAVIRTAQSLTQSLTSLRSGWKTIGALVMPMLMIQGYKKGLIKFSIITCR | |
| SEQ ID NO:28 | DWSRFVAPFWPFAVIRSAFTWKGLSSLLSSGQKTIKALAMPLMIEGYKKDLIKFAIITCR | |
| SEQ ID NO:08 | DWSRFVAPFWPFAVIRSAFTWKGLSSLLSSGKLGI-----YIAFQKQTPPSSSIATCK | |
| SEQ ID NO:22 | DWSENVAPFWPFAVIRSAFTWKGLSSLLSSGKLGI-----YIAFQKQTPPSSSIATCK | |
| SEQ ID NO:24 | ----- | |
| SEQ ID NO:26 | DWSENVAPFWPFAVIRSAFTWKGLTSLRSGWETVRGAMVMPPLVIEGYKKGLIKFPIITCR | 360 |
| | | 301 |

FIGURE 1

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SEQ ID NO:39 KPLV-----  
SEQ ID NO:40 KPL-----  
SEQ ID NO:38 KPQAAIEGEPEEAAPSVE.-  
SEQ ID NO:28 K-----PE.-  
SEQ ID NO:08 SYVTDHYFHTR.-  
SEQ ID NO:22 KPGAA-.MA---HAALLHC  
SEQ ID NO:24 -----  
SEQ ID NO:26 KPETT-----Q.-  
361 380
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FIGURE 2

| | | |
|---------------|--|-----|
| SEQ ID NO: 41 | MPPPTTPAATGAAAATPEHARPH-----RMVRENPRSDRFHTLSFHHVEFWCADAASA | 60 |
| SEQ ID NO: 43 | MGHQNAAVSENQNHDDGAASSPGFKLVGFSEKVRKNPKSKDKFKVKRFHHIEFWCGDATNV | |
| SEQ ID NO: 42 | MGKKQSEAEILSS-NSSNTSPATFKLVGFNNFVRANPKSDHFAVKRFHHIEFWCGDATNT | |
| SEQ ID NO: 36 | MPIPMCNEIQAQA-QAQAQAQPGFKLVGFKNFVRTNPKSDRFQVNRHHIEFWCTDATNA | |
| SEQ ID NO: 38 | MPPPTTPAATGAAA-VTPEHARPR-----RMVRENPRSDRFHTLAFHHVEFWCADAASA | |
| SEQ ID NO: 32 | MGK-QTTTSATAA-DGSKDAHAEFKLVGFKNFVRTNPKSDHFCVHREHHIEFWCGDATNT | 1 |
| | | 61 |
| SEQ ID NO: 41 | AGRFAFALGAPLAARSDLSTGNSAHASQLLRSGSLAFLFTAPYANG-----CDAATASL | 120 |
| SEQ ID NO: 43 | ARRFSWGLGMRFSAKSDLSTGNMVHASLYLLTSGDLRFLFTAPYSPSLSAGEIKPTTTASI | |
| SEQ ID NO: 42 | SRRFSWGLGMPLVAKSDLSTGNSVHASLYLRSANLSFVFTAPYSPSTTSS-G---SAAI | |
| SEQ ID NO: 36 | SRRFSWGLGMPPIVAKSDLSTGNQIHASLYLLRSGDLSELFSAFYSPSLSAGS-SAASSASI | |
| SEQ ID NO: 38 | AGRFAFALGAPLAARSDLSTGNSVHASQLLRSGNLAFLLFTAPYANG-----CDAATASL | |
| SEQ ID NO: 32 | AKRFSWGLGMPLVAKSDLSTGNSAHASLYLLRSGELNFLTSPYSPSISAPS-----SAAI | 61 |
| | | 121 |
| SEQ ID NO: 41 | PSFSADAARRFSADHGI AVR SVALRVADAAEAFRASRRRGARPAFAPVDLGRGFA-FAEV | |
| SEQ ID NO: 43 | PSFDHGSCRSFFSSHGLGVRAVAIEVEDAESAFSISVANGAIPSSPPIVLNEAVT-IAEV | |
| SEQ ID NO: 42 | PSFSASGFHSFAAKHGLAVRAIALEVADVAFAFEASVARGARPAAPVEL-DDQAWLAEV | |
| SEQ ID NO: 36 | PSFDAATCLAEFAAKHGFVRAIALEVADAEAAFSASVAKGAEPASPPV-LVDDRTGFAEV | |
| SEQ ID NO: 38 | PSFSADAARQFSADHGLAVRSIALRVADAAEAFRASVDGGARPAFSPVDLGRGFG-FAEV | |
| SEQ ID NO: 32 | PSFSFSTYQSFSTSSHGLAVRAVAIQVDSAFSAYSASISRGAKPVSAPIILLSDNKTIAEV | 180 |
| | | 121 |

FIGURE 2

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SEQ ID NO:41  ELYGDEVVLRVFSH-PDGTDP-----FLPGFEGVTNPDA---VDYGLTRFDHVVGNVNP
SEQ ID NO:43  KLYGDEVVLRVVSYKAEDTEKSE-----FLPGFERVEDASSFP-LDYGIRRLDHAVGNVNP
SEQ ID NO:42  ELYGDEVVLRVFSFGRE-----EGLFLPGFEAVEGTASFPDLDYGIRRLDHAVGNVT
SEQ ID NO:36  RLYGDEVVLRVVSYKDAAPQAPHADPSRWFLPGFEAAASSSFPELDYGIRRLDHAVGNVNP
SEQ ID NO:38  ELYGDEVVLRVFSH-PDGRDVP-----FLPGFEGVSNPDA---VDYGLTRFDHVVGNVNP
SEQ ID NO:32  HLYGDSVLRVFSYGDNG-----TGPDCWFPGFEPVDDQMSYKELDYGIRRLDHAVGNVNP
                181                                240

SEQ ID NO:41  ELAPAAAYIAGFTGFHFAEFTAEADVGTESGLNSVVLANNSEGVLLPLNEPVHGTKRRS
SEQ ID NO:43  ELGPALTYVAGFTGFHQFAEFTADVDVGTAEGLNSAVLASNDEMVLPLINEPVHGTKRKS
SEQ ID NO:42  ELGPVVEYIKGFTGFHFAEFTAEADVGTESGLNSVVLANNSEMVLLPLNEPVYGTKRKS
SEQ ID NO:36  ELAPAVRYLKGFSGFHFAEFTAEADVGTESGLNSVVLANNSETVLLPLNEPVYGTKRKS
SEQ ID NO:38  ELAPAAAYVAGFTGFHFAEFTTEDVGTAEGLNSMVLANNSEGVLLPLNEPVHGTKRRS
SEQ ID NO:32  ELGPVVDYLLKFTGFHFAEFTSEDVGTAEGLNSMVLANNENVLLPLNEPVFGTKRKS
                241                                300

SEQ ID NO:41  QIQTFLHHGGPGVQVQHIAVASSDVLRTLRKMRRARSAMGGFDLPPPLPKYYEGVRRLAGD
SEQ ID NO:43  QIQTYLEHNEGAGLQHLALMSEDI FRTLREMRKRSSIGGDFMPSPPPTYQNKKRVGD
SEQ ID NO:42  QIQTYLEHNEGAGVQHLALVSEDI FRTLREMRKRSCLGGEFMPSPPTTYKNLKNRVGD
SEQ ID NO:36  QIETYLEHNEGAGVQHLALVTHDI FTTLREMRKRSSFLLGGFEFMPSPPTTYANLHNRAAD
SEQ ID NO:38  QIQTFLHHGGSGVQVQHIAVASSDVLRTLREMRARSAMGGFDLPPPLPKYYEGVRRLAGD
SEQ ID NO:32  QIQTYLEHNEGPGVQHLALVSEDI FNTLREMRKRSGVGGFEFMPSPPLTYKNLKNRAGD
                301                                360

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FIGURE 2

SEQ ID NO: 41 VLSEAQIKECQELGVLDVDRDDQGVLLQIFTKPVGDRPTLFLEMIQRIIGCMKDERGEEYQ
SEQ ID NO: 43 VLSDDQIKECEEELGILVDRDDQGVLLQIFTKPLGDRPTIFIEIIQRVGCMKDEEGKAYQ
SEQ ID NO: 42 VLSDEQIKECEDLGVLDVDRDDQGVLLQIFTKPVGDRPTLFIEIIQRVGCMKDDAGQMYQ
SEQ ID NO: 36 VLTVDQIKQCEEELGILVDRDDQGVLLQIFTKPVGDRPTIFIEIIQRIIGCMVEDEEGKVYQ
SEQ ID NO: 38 VLSEAQIKECQELGVLDVDRDDQGVLLQIFTKPVGDRPTLFLEMIQRIIGCMKDERGEEYQ
SEQ ID NO: 32 VLRDEQIEECEKLGILVDRDDQGVLLQIFTKPVGDRPTLFIEIIQRIIGCMKDEQKLYQ
361 420

SEQ ID NO: 41 KGGCGGFGKGNFSELFKSIEDYEKSLEAKQSAAVQG-S
SEQ ID NO: 43 SGGCGGFGKGNFSELFKSIEEYEKTLQAKLVG-----
SEQ ID NO: 42 KGGCGGFGKGNFSELFKSIEEYEKTLQAKQITGSA-AA
SEQ ID NO: 36 KGACGGFGKGNFSELFKSIEEYEKTLQAKR-----TA.
SEQ ID NO: 38 KGGCGGFGKGNFSELFKSIEDYEKSLEAKQSAAVQGS.
SEQ ID NO: 32 KSGCGGFGKGNFSELFKSIEEYEKMLEAKQVTTETASA.
421 458

Figure 3

